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0530

# 8



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/082,894

DATE: 06/04/2002  
TIME: 12:37:17

Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF3\06042002\J082894.raw

4 <110> APPLICANT: Kloek, Andrew P.  
5 Williams, Deryck Jeremy  
6 Salmon, Brandy Leigh  
7 Bradley, John D.  
9 <120> TITLE OF INVENTION: NEMATODE PGM-LIKE SEQUENCES  
11 <130> FILE REFERENCE: 12557-003001  
13 <140> CURRENT APPLICATION NUMBER: US 10/082,894  
14 <141> CURRENT FILING DATE: 2002-02-26  
16 <150> PRIOR APPLICATION NUMBER: US 60/271,781  
17 <151> PRIOR FILING DATE: 2001-02-27  
19 <160> NUMBER OF SEQ ID NOS: 14  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 1719  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Meloidogyne incognita PGM  
28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (22)...(1599)  
32 <400> SEQUENCE: 1

ENTERED

33	gtttaattac ccaagtttga g atg gac aaa tat caa aat gtt caa caa aaa	51
34	Met Asp Lys Tyr Gln Asn Val Gln Gln Lys	
35	1 5 10	
37	gtc tgt ctt gta gtt att gat gga tgg ggc ctt tcc gat gaa caa cac	99
38	Val Cys Leu Val Val Ile Asp Gly Trp Gly Leu Ser Asp Glu Gln His	
39	15 20 25	
41	ggg aat gca att gct aaa gct aaa acg cct att atg gac aaa ctt tgt	147
42	Gly Asn Ala Ile Ala Lys Ala Thr Pro Ile Met Asp Lys Leu Cys	
43	30 35 40	
45	tct gga aat tgg caa aaa ttg gaa gca cac ggt ctt cat gtt gga ttg	195
46	Ser Gly Asn Trp Gln Lys Leu Glu Ala His Gly Leu His Val Gly Leu	
47	45 50 55	
49	cca gaa ggc tta atg gga aat tct gaa gtt gga cat ttg aat ata gga	243
50	Pro Glu Gly Leu Met Gly Asn Ser Glu Val Gly His Leu Asn Ile Gly	
51	60 65 70	
53	gct gga aga gtt att tat caa gat att gtt cga att aat ttg gct gtt	291
54	Ala Gly Arg Val Ile Tyr Gln Asp Ile Val Arg Ile Asn Leu Ala Val	
55	75 80 85 90	
57	caa cga aac gag ttt gtt aca aat cct cag att gtt gca tca gct gag	339
58	Gln Arg Asn Glu Phe Val Thr Asn Pro Gln Ile Val Ala Ser Ala Glu	
59	95 100 105	
61	cgt gca aag aag ggg agt ggt cga ttg cat tta tta gga ctg gtt agc	387
62	Arg Ala Lys Lys Gly Ser Gly Arg Leu His Leu Leu Gly Leu Val Ser	

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63	110	115	120	
65	gat ggt ggt gtc cac tct cat att gat cat ctt ttt gcg ttg ata cgt			435
66	Asp Gly Gly Val His Ser His Ile Asp His Leu Phe Ala Leu Ile Arg			
67	125	130	135	
69	gca ttt aaa caa tta caa gtg cca aag gtt ttc att cac ttt ttt gct			483
70	Ala Phe Lys Gln Leu Gln Val Pro Lys Val Phe Ile His Phe Phe Ala			
71	140	145	150	
73	gat ggt cga gat act tcg cca aca agt gga gct ggt tat ctt gaa caa			531
74	Asp Gly Arg Asp Thr Ser Pro Thr Ser Gly Ala Gly Tyr Leu Glu Gln			
75	155	160	165	170
77	ctt ctt caa ttt att gct tcg gaa aag tac gga gaa ttg gct act att			579
78	Leu Leu Gln Phe Ile Ala Ser Glu Lys Tyr Gly Glu Leu Ala Thr Ile			
79	175	180	185	
81	act gga cgt tat tat gca atg gat agg gac aaa aga tgg gag cgt att			627
82	Thr Gly Arg Tyr Tyr Ala Met Asp Arg Asp Lys Arg Trp Glu Arg Ile			
83	190	195	200	
85	aag atg gct tat gag gca att gtt gga ggt att gga caa aaa gcc acc			675
86	Lys Met Ala Tyr Glu Ala Ile Val Gly Gly Ile Gly Gln Lys Ala Thr			
87	205	210	215	
89	gtt gat aag gct gtc gat gtt aga gag cga tat gct caa tct gag			723
90	Val Asp Lys Ala Val Asp Val Val Arg Glu Arg Tyr Ala Gln Ser Glu			
91	220	225	230	
93	act gac gaa ttt ctg aaa cca att gtt ttt tcg gac gat ggg cga gta			771
94	Thr Asp Glu Phe Leu Lys Pro Ile Val Phe Ser Asp Asp Gly Arg Val			
95	235	240	245	250
97	aaa gat gac gat act ctt att ttc ttc aat tat cgt gct gat cgt atg			819
98	Lys Asp Asp Asp Thr Leu Ile Phe Phe Asn Tyr Arg Ala Asp Arg Met			
99	255	260	265	
101	cgt caa att tgt gaa tgt ttg ggt ctc gaa cgt tat aaa gat ctt aat			867
102	Arg Gln Ile Cys Glu Cys Leu Gly Leu Glu Arg Tyr Lys Asp Leu Asn			
103	270	275	280	
105	agt tcg gtt cct cac cct aaa aat att cag att agt ggg atg acc caa			915
106	Ser Ser Val Pro His Pro Lys Asn Ile Gln Ile Ser Gly Met Thr Gln			
107	285	290	295	
109	tac aat aaa gag ttt cca ttt cca tcg tta ttc cca cct gtg act cat			963
110	Tyr Asn Lys Glu Phe Pro Phe Pro Ser Leu Phe Pro Pro Val Thr His			
111	300	305	310	
113	act aat gtg ctt gct gaa tgg ctt gct tct caa gga gtt act caa ttt			1011
114	Thr Asn Val Leu Ala Glu Trp Leu Ala Ser Gln Gly Val Thr Gln Phe			
115	315	320	325	330
117	cac tgt gcg gaa act gag aag tat cct cat gtt acc ttc ttc ttt aat			1059
118	His Cys Ala Glu Thr Glu Lys Tyr Pro His Val Thr Phe Phe Asn			
119	335	340	345	
121	ggt ggt cga gaa gtt caa ttc caa gat gaa gag cgt tgt atg gtt ccg			1107
122	Gly Gly Arg Glu Val Gln Phe Gln Asp Glu Glu Arg Cys Met Val Pro			
123	350	355	360	
125	tca cca aaa gaa gtt gct aca tat gat tta aaa cca gaa atg aat gct			1155
126	Ser Pro Lys Glu Val Ala Thr Tyr Asp Leu Lys Pro Glu Met Asn Ala			
127	365	370	375	

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129	gct	gga	gtt	gcc	gaa	aaa	atg	gtc	gag	caa	att	gag	tca	ggc	agg	cat	1203
130	Ala	Gly	Val	Ala	Glu	Lys	Met	Val	Glu	Gln	Ile	Glu	Ser	Gly	Arg	His	
131	380				385					390							
133	cct	ttg	gtt	atg	tgc	aat	ttt	gcg	cct	cct	gac	atg	gtt	gga	cat	act	1251
134	Pro	Leu	Val	Met	Cys	Asn	Phe	Ala	Pro	Pro	Asp	Met	Val	Gly	His	Thr	
135	395				400					405					410		
137	ggt	aaa	ttt	gaa	cct	gcc	gtc	aaa	gca	tgt	caa	gct	act	gac	gag	gca	1299
138	Gly	Lys	Phe	Glu	Pro	Ala	Val	Lys	Ala	Cys	Gln	Ala	Thr	Asp	Glu	Ala	
139					415					420					425		
141	att	gga	aag	ata	ttt	gaa	gca	tgc	caa	act	tat	aat	tac	gtt	ctt	atg	1347
142	Ile	Gly	Lys	Ile	Phe	Glu	Ala	Cys	Gln	Thr	Tyr	Asn	Tyr	Val	Leu	Met	
143					430					435					440		
145	gtt	act	tcc	gat	cat	gga	aat	gct	gag	aag	atg	att	gct	ccc	gat	ggt	1395
146	Val	Thr	Ser	Asp	His	Gly	Asn	Ala	Glu	Lys	Met	Ile	Ala	Pro	Asp	Gly	
147					445					450					455		
149	agt	gaa	cat	act	gca	cat	acc	tgc	aat	ttg	gtc	cca	ttt	act	tgc	tct	1443
150	Ser	Glu	His	Thr	Ala	His	Thr	Cys	Asn	Leu	Val	Pro	Phe	Thr	Cys	Ser	
151					460					465					470		
153	tcc	aaa	aca	ttt	gtt	ttt	aaa	tcg	act	cca	cct	act	gga	gat	gat	ggc	1491
154	Ser	Lys	Thr	Phe	Val	Phe	Lys	Ser	Thr	Pro	Pro	Thr	Gly	Asp	Asp	Gly	
155					475					480					485		
157	aaa	gaa	cgt	gca	cga	gcc	tta	cgt	gat	gtt	gca	ccg	act	gtt	cta	caa	1539
158	Lys	Glu	Arg	Ala	Arg	Ala	Leu	Arg	Asp	Val	Ala	Pro	Thr	Val	Leu	Gln	
159					495					500					505		
161	tta	atg	ggc	tta	cct	gta	ccg	ccg	gag	atg	gat	ggc	gtt	cct	tta	ctt	1587
162	Leu	Met	Gly	Leu	Pro	Val	Pro	Pro	Glu	Met	Asp	Gly	Val	Pro	Leu	Leu	
163					510					515					520		
165	gaa	cag	aga	gga	taagaaggta	attgacaata	ggaaataaaat	atgagctgct									1639
166	Glu	Gln	Arg	Gly													
167				525													
169	attacaagca	atttaaaaaa	tttttagtaaa	acgagtaatt	tttgatatat	acatattttag											1699
170	aaatctccgt	tataaaaatt															1719
172	<210>	SEQ ID NO:	2														
173	<211>	LENGTH:	526														
174	<212>	TYPE:	PRT														
175	<213>	ORGANISM:	Meloidogyne incognita	PGM													
177	<400>	SEQUENCE:	2														
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179	1				5					10					15		
180	Asp	Gly	Trp	Gly	Leu	Ser	Asp	Glu	Gln	His	Gly	Asn	Ala	Ile	Ala	Lys	
181					20					25					30		
182	Ala	Lys	Thr	Pro	Ile	Met	Asp	Lys	Leu	Cys	Ser	Gly	Asn	Trp	Gln	Lys	
183					35					40					45		
184	Leu	Glu	Ala	His	Gly	Leu	His	Val	Gly	Leu	Pro	Glu	Gly	Leu	Met	Gly	
185					50					55					60		
186	Asn	Ser	Glu	Val	Gly	His	Leu	Asn	Ile	Gly	Ala	Gly	Arg	Val	Ile	Tyr	
187					65					70					75		80
188	Gln	Asp	Ile	Val	Arg	Ile	Asn	Leu	Ala	Val	Gln	Arg	Asn	Glu	Phe	Val	
189					85					90					95		

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190 Thr Asn Pro Gln Ile Val Ala Ser Ala Glu Arg Ala Lys Lys Gly Ser  
 191 100 105 110  
 192 Gly Arg Leu His Leu Leu Gly Leu Val Ser Asp Gly Gly Val His Ser  
 193 115 120 125  
 194 His Ile Asp His Leu Phe Ala Leu Ile Arg Ala Phe Lys Gln Leu Gln  
 195 130 135 140  
 196 Val Pro Lys Val Phe Ile His Phe Ala Asp Gly Arg Asp Thr Ser  
 197 145 150 155 160  
 198 Pro Thr Ser Gly Ala Gly Tyr Leu Glu Gln Leu Leu Gln Phe Ile Ala  
 199 165 170 175  
 200 Ser Glu Lys Tyr Gly Glu Leu Ala Thr Ile Thr Gly Arg Tyr Tyr Ala  
 201 180 185 190  
 202 Met Asp Arg Asp Lys Arg Trp Glu Arg Ile Lys Met Ala Tyr Glu Ala  
 203 195 200 205  
 204 Ile Val Gly Gly Ile Gly Gln Lys Ala Thr Val Asp Lys Ala Val Asp  
 205 210 215 220  
 206 Val Val Arg Glu Arg Tyr Ala Gln Ser Glu Thr Asp Glu Phe Leu Lys  
 207 225 230 235 240  
 208 Pro Ile Val Phe Ser Asp Asp Gly Arg Val Lys Asp Asp Asp Thr Leu  
 209 245 250 255  
 210 Ile Phe Phe Asn Tyr Arg Ala Asp Arg Met Arg Gln Ile Cys Glu Cys  
 211 260 265 270  
 212 Leu Gly Leu Glu Arg Tyr Lys Asp Leu Asn Ser Ser Val Pro His Pro  
 213 275 280 285  
 214 Lys Asn Ile Gln Ile Ser Gly Met Thr Gln Tyr Asn Lys Glu Phe Pro  
 215 290 295 300  
 216 Phe Pro Ser Leu Phe Pro Pro Val Thr His Thr Asn Val Leu Ala Glu  
 217 305 310 315 320  
 218 Trp Leu Ala Ser Gln Gly Val Thr Gln Phe His Cys Ala Glu Thr Glu  
 219 325 330 335  
 220 Lys Tyr Pro His Val Thr Phe Phe Asn Gly Gly Arg Glu Val Gln  
 221 340 345 350  
 222 Phe Gln Asp Glu Glu Arg Cys Met Val Pro Ser Pro Lys Glu Val Ala  
 223 355 360 365  
 224 Thr Tyr Asp Leu Lys Pro Glu Met Asn Ala Ala Gly Val Ala Glu Lys  
 225 370 375 380  
 226 Met Val Glu Gln Ile Glu Ser Gly Arg His Pro Leu Val Met Cys Asn  
 227 385 390 395 400  
 228 Phe Ala Pro Pro Asp Met Val Gly His Thr Gly Lys Phe Glu Pro Ala  
 229 405 410 415  
 230 Val Lys Ala Cys Gln Ala Thr Asp Glu Ala Ile Gly Lys Ile Phe Glu  
 231 420 425 430  
 232 Ala Cys Gln Thr Tyr Asn Tyr Val Leu Met Val Thr Ser Asp His Gly  
 233 435 440 445  
 234 Asn Ala Glu Lys Met Ile Ala Pro Asp Gly Ser Glu His Thr Ala His  
 235 450 455 460  
 236 Thr Cys Asn Leu Val Pro Phe Thr Cys Ser Ser Lys Thr Phe Val Phe  
 237 465 470 475 480  
 238 Lys Ser Thr Pro Pro Thr Gly Asp Asp Gly Lys Glu Arg Ala Arg Ala

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239                   485                   490                   495  
 240 Leu Arg Asp Val Ala Pro Thr Val Leu Gln Leu Met Gly Leu Pro Val  
 241               500               505               510  
 242 Pro Pro Glu Met Asp Gly Val Pro Leu Leu Glu Gln Arg Gly  
 243               515               520               525  
 245 <210> SEQ ID NO: 3  
 246 <211> LENGTH: 539  
 247 <212> TYPE: PRT  
 248 <213> ORGANISM: Caenorhabidits elegans PGM  
 250 <400> SEQUENCE: 3  
 251 Met Phe Val Ala Leu Gly Ala Gln Ile Tyr Arg Gln Tyr Phe Gly Arg  
 252   1               5               10               15  
 253 Arg Gly Met Ala Met Ala Asn Asn Ser Ser Val Ala Asn Lys Val Cys  
 254       20               25               30  
 255 Leu Ile Val Ile Asp Gly Trp Gly Val Ser Glu Asp Pro Tyr Gly Asn  
 256       35               40               45  
 257 Ala Ile Leu Asn Ala Gln Thr Pro Val Met Asp Lys Leu Cys Ser Gly  
 258       50               55               60  
 259 Asn Trp Ala Gln Ile Glu Ala His Gly Leu His Val Gly Leu Pro Glu  
 260       65               70               75               80  
 261 Gly Leu Met Gly Asn Ser Glu Val Gly His Leu Asn Ile Gly Ala Gly  
 262       85               90               95  
 263 Arg Val Ile Tyr Gln Asp Ile Val Arg Ile Asn Leu Ala Val Lys Asn  
 264       100               105               110  
 265 Asn Lys Phe Val Thr Asn Glu Ser Leu Val Asp Ala Cys Asp Arg Ala  
 266       115               120               125  
 267 Lys Asn Gly Asn Gly Arg Leu His Leu Ala Gly Leu Val Ser Asp Gly  
 268       130               135               140  
 269 Gly Val His Ser His Ile Asp His Met Phe Ala Leu Val Lys Ala Ile  
 270       145               150               155               160  
 271 Lys Glu Leu Gly Val Pro Glu Leu Tyr Leu His Phe Tyr Gly Asp Gly  
 272       165               170               175  
 273 Arg Asp Thr Ser Pro Asn Ser Gly Val Gly Phe Leu Glu Gln Thr Leu  
 274       180               185               190  
 275 Glu Phe Leu Glu Lys Thr Thr Gly Tyr Gly Lys Leu Ala Thr Val Val  
 276       195               200               205  
 277 Gly Arg Tyr Tyr Ala Met Asp Arg Asp Asn Arg Trp Glu Arg Ile Asn  
 278       210               215               220  
 279 Val Ala Tyr Glu Ala Met Ile Gly Gly Val Gly Glu Thr Ser Asp Glu  
 280       225               230               235               240  
 281 Ala Gly Val Val Glu Val Val Arg Lys Arg Tyr Ala Ala Asp Glu Thr  
 282       245               250               255  
 283 Asp Glu Phe Leu Lys Pro Ile Ile Leu Gln Gly Glu Lys Gly Arg Val  
 284       260               265               270  
 285 Gln Asn Asp Asp Thr Ile Ile Phe Phe Asp Tyr Arg Ala Asp Arg Met  
 286       275               280               285  
 287 Arg Glu Ile Ser Ala Ala Met Gly Met Asp Arg Tyr Lys Asp Cys Asn  
 288       290               295               300  
 289 Ser Lys Leu Ala His Pro Ser Asn Leu Gln Val Tyr Gly Met Thr Gln

**VERIFICATION SUMMARY**  
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